



E-utilities Quick Start

Eric Sayers, PhD^{✉1}

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Release Notes

Please see our [Release Notes](#) for details on recent changes and updates.

Announcement

On December 1, 2018, NCBI will begin enforcing the use of new API keys for E-utility calls. Please see [Chapter 2](#) for more details about this important change.

Introduction

This chapter provides a brief overview of basic E-utility functions along with examples of URL calls. Please see [Chapter 2](#) for a general introduction to these utilities and [Chapter 4](#) for a detailed discussion of syntax and parameters.

Examples include live URLs that provide sample outputs.

All E-utility calls share the same base URL:

`https://eutils.ncbi.nlm.nih.gov/entrez/eutils/`

Searching a Database

Basic Searching

`esearch.fcgi?db=<database>&term=<query>`

Input: Entrez database (&db); Any Entrez text query (&term)

Output: List of UIDs matching the Entrez query

Example: Get the PubMed IDs (PMIDs) for articles about breast cancer published in Science in 2008

[https://eutils.ncbi.nlm.nih.gov/entrez/eutils/esearch.fcgi?db=pubmed&term=science\[journal\]+AND+breast+cancer+AND+2008\[pdat\]](https://eutils.ncbi.nlm.nih.gov/entrez/eutils/esearch.fcgi?db=pubmed&term=science[journal]+AND+breast+cancer+AND+2008[pdat])

Storing Search Results

```
eSearch.fcgi?db=<database>&term=<query>&usehistory=y
```

Input: Any Entrez text query (&term); Entrez database (&db); &usehistory=y

Output: Web environment (&WebEnv) and query key (&query_key) parameters specifying the location on the Entrez history server of the list of UIDs matching the Entrez query

Example: Get the PubMed IDs (PMIDs) for articles about breast cancer published in Science in 2008, and store them on the Entrez history server for later use

```
https://eutils.ncbi.nlm.nih.gov/entrez/eutils/eSearch.fcgi?db=pubmed&term=science[journal]
+AND+breast+cancer+AND+2008[pdat]&usehistory=y
```

Associating Search Results with Existing Search Results

```
eSearch.fcgi?db=<database>&term=<query1>&usehistory=y
```

```
# eSearch produces WebEnv value ($web1) and QueryKey value ($key1)
```

```
eSearch.fcgi?db=<database>&term=<query2>&usehistory=y&WebEnv=$web1
```

```
# eSearch produces WebEnv value ($web2) that contains the results
of both searches ($key1 and $key2)
```

Input: Any Entrez text query (&term); Entrez database (&db); &usehistory=y; Existing web environment (&WebEnv) from a prior E-utility call

Output: Web environment (&WebEnv) and query key (&query_key) parameters specifying the location on the Entrez history server of the list of UIDs matching the Entrez query

For More Information

Please see [ESearch In-Depth](#) for a full description of ESearch.

Sample ESearch Output

```
<?xml version="1.0" ?>
<!DOCTYPE eSearchResult PUBLIC "-//NLM//DTD eSearchResult, 11 May 2002//EN"
  "https://www.ncbi.nlm.nih.gov/entrez/query/DTD/eSearch_020511.dtd">
<eSearchResult>
<Count>255147</Count> # total number of records matching query
<RetMax>20</RetMax># number of UIDs returned in this XML; default=20
<RetStart>0</RetStart># index of first record returned; default=0
<QueryKey>1</QueryKey># QueryKey, only present if &usehistory=y
<WebEnv>0193yIkBjmM60UBXuvBvPfbIq8-9nIslDXuMP0hhuMH-
8GjCz7F_Dz1XL6z@397033B29A81FB01_0038SID</WebEnv>
  # WebEnv; only present if &usehistory=y
  <IdList>
<Id>229486465</Id> # list of UIDs returned
<Id>229486321</Id>
<Id>229485738</Id>
<Id>229470359</Id>
<Id>229463047</Id>
<Id>229463037</Id>
<Id>229463022</Id>
<Id>229463019</Id>
```

```

<Id>229463007</Id>
<Id>229463002</Id>
<Id>229463000</Id>
<Id>229462974</Id>
<Id>229462961</Id>
<Id>229462956</Id>
<Id>229462921</Id>
<Id>229462905</Id>
<Id>229462899</Id>
<Id>229462873</Id>
<Id>229462863</Id>
<Id>229462862</Id>
</IdList>
<TranslationSet>          # details of how Entrez translated the query
  <Translation>
    <From>mouse[orgn]</From>
    <To>"Mus musculus"[Organism]</To>
  </Translation>
</TranslationSet>
<TranslationStack>
  <TermSet>
    <Term>"Mus musculus"[Organism]</Term>
    <Field>Organism</Field>
    <Count>255147</Count>
    <Explode>Y</Explode>
  </TermSet>
  <OP>GROUP</OP>
</TranslationStack>
<QueryTranslation>"Mus musculus"[Organism]</QueryTranslation>
</eSearchResult>

```

Searching PubMed with Citation Data

```
ecitmatch.cgi?db=pubmed&rettype=xml&bdata=<citations>
```

Input: List of citation strings separated by a carriage return (%0D), where each citation string has the following format:

```
journal_title|year|volume|first_page|author_name|your_key|
```

Output: A list of citation strings with the corresponding PubMed ID (PMID) appended.

Example: Search PubMed for the following citations:

Art1: Mann, BJ. (1991) *Proc. Natl. Acad. Sci. USA*. 88:3248

Art2: Palmenberg, AC. (1987) *Science* 235:182

[https://eutils.ncbi.nlm.nih.gov/entrez/eutils/ecitmatch.cgi?](https://eutils.ncbi.nlm.nih.gov/entrez/eutils/ecitmatch.cgi?db=pubmed&retmode=xml&bdata=proc+natl+acad+sci+u+s+a|1991|88|3248|mann+bj|Art1|%0Dscience|1987|235|182|palmenberg+ac|Art2)

[db=pubmed&retmode=xml&bdata=proc+natl+acad+sci+u+s+a|1991|88|3248|mann+bj|Art1|%0Dscience|1987|235|182|palmenberg+ac|Art2](https://eutils.ncbi.nlm.nih.gov/entrez/eutils/ecitmatch.cgi?db=pubmed&retmode=xml&bdata=proc+natl+acad+sci+u+s+a|1991|88|3248|mann+bj|Art1|%0Dscience|1987|235|182|palmenberg+ac|Art2)

Sample Output (the PMIDs appear in the rightmost field):

```
proc natl acad sci u s a|1991|88|3248|mann bj|Art1|2014248
science|1987|235|182|palmenberg ac|Art2|3026048
```

Please see [ECitMatch In-Depth](#) for a full description of ECitMatch.

Uploading UIDs to Entrez

Basic Uploading

```
epost.fcgi?db=<database>&id=<uid_list>
```

Input: List of UIDs (&id); Entrez database (&db)

Output: Web environment (&WebEnv) and query key (&query_key) parameters specifying the location on the Entrez history server of the list of uploaded UIDs

Example: Upload five Gene IDs (7173,22018,54314,403521,525013) for later processing.

<https://eutils.ncbi.nlm.nih.gov/entrez/eutils/epost.fcgi?db=gene&id=7173,22018,54314,403521,525013>

Associating a Set of UIDs with Previously Posted Sets

```
epost.fcgi?db=<database1>&id=<uid_list1>
```

epost produces WebEnv value (\$web1) and QueryKey value (\$key1)

```
epost.fcgi?db=<database2>&id=<uid_list2>&WebEnv=$web1
```

epost produces WebEnv value (\$web2) that contains the results of both posts (\$key1 and \$key2)

Input: List of UIDs (&id); Entrez database (&db); Existing web environment (&WebEnv)

Output: Web environment (&WebEnv) and query key (&query_key) parameters specifying the location on the Entrez history server of the list of uploaded UIDs

For More Information

Please see [EPost In-Depth](#) for a full description of EPost.

Sample EPost Output

```
<?xml version="1.0"?>
<!DOCTYPE ePostResult PUBLIC "-//NLM//DTD ePostResult, 11 May 2002//EN"
  "https://www.ncbi.nlm.nih.gov/entrez/query/DTD/ePost_020511.dtd">
<ePostResult>
<QueryKey>1</QueryKey>
<WebEnv>NCID_01_268116914_130.14.18.47_9001_1241798628</WebEnv>
</ePostResult>
```

Downloading Document Summaries

Basic Downloading

```
esummary.fcgi?db=<database>&id=<uid_list>
```

Input: List of UIDs (&id); Entrez database (&db)

Output: XML DocSums

Example: Download DocSums for these protein GIs: 6678417,9507199,28558982,28558984,28558988,28558990

<https://eutils.ncbi.nlm.nih.gov/entrez/eutils/esummary.fcgi?db=protein&id=6678417,9507199,28558982,28558984,28558988,28558990>

Downloading Data From a Previous Search

```
esearch.fcgi?db=<database>&term=<query>&usehistory=y
```

```
# esearch produces WebEnv value ($web1) and QueryKey value ($key1)
```

```
esummary.fcgi?db=<database>&query_key=$key1&WebEnv=$web1
```

Input: Web environment (&WebEnv) and query key (&query_key) representing a set of Entrez UIDs on the Entrez history server

Output: XML DocSums

Sample ESummary Output

The output of ESummary is a series of XML “DocSums” (Document Summaries), the format of which depends on the database. Below is an example DocSum for Entrez Protein.

```
<?xml version="1.0"?>
<!DOCTYPE eSummaryResult PUBLIC "-//NLM//DTD eSummaryResult, 29 October
 2004//EN" "https://www.ncbi.nlm.nih.gov/entrez/query/DTD/eSummary_
041029.dtd">
<eSummaryResult>
<DocSum>
<Id>15718680</Id>
<Item Name="Caption" Type="String">NP_005537</Item>
<Item Name="Title" Type="String">IL2-inducible T-cell kinase [Homo
sapiens]</Item>
<Item Name="Extra"
Type="String">gi|15718680|ref|NP_005537.3|[15718680]</Item>
<Item Name="Gi" Type="Integer">15718680</Item>
<Item Name="CreateDate" Type="String">1999/06/09</Item>
<Item Name="UpdateDate" Type="String">2009/04/05</Item>
<Item Name="Flags" Type="Integer">512</Item>
<Item Name="TaxId" Type="Integer">9606</Item>
<Item Name="Length" Type="Integer">620</Item>
<Item Name="Status" Type="String">live</Item>
<Item Name="ReplacedBy" Type="String"></Item>
<Item Name="Comment" Type="String"><![CDATA[ ]]></Item>
</DocSum>
</eSummaryResult>
```

Sample ESummary version 2.0 Output

Version 2.0 of ESummary is an alternate XML presentation of Entrez DocSums. To retrieve version 2.0 DocSums, the URL should contain the &version parameter with an assigned value of ‘2.0’. Each Entrez database provides its own unique DTD for version 2.0 DocSums, and a link to the relevant DTD is provided in the header of the version 2.0 XML.

```
esummary.fcgi?db=<database>&id=<uid_list>&version=2.0
```

Below is an example version 2.0 DocSum from Entrez Protein (the same record as shown above in the default DocSum XML).

```
<?xml version="1.0"?>
<!DOCTYPE eSummaryResult PUBLIC "-//NLM//DTD eSummaryResult//EN" "https://
www.ncbi.nlm.nih.gov/entrez/query/DTD/eSummaryDTD/eSummary_protein.dtd">
<eSummaryResult>
  <DocumentSummarySet status="OK">
    <DocumentSummary uid="15718680">
      <Caption>NP_005537</Caption>
      <Title>tyrosine-protein kinase ITK/TSK [Homo sapiens]</Title>
      <Extra>gi|15718680|ref|NP_005537.3|</Extra>
      <Gi>15718680</Gi>

      <CreateDate>1999/06/09</CreateDate>
      <UpdateDate>2011/10/09</UpdateDate>
      <Flags>512</Flags>
      <TaxId>9606</TaxId>
      <Slen>620</Slen>

      <Biomol/>

      <MolType>aa</MolType>
      <Topology>linear</Topology>
      <SourceDb>refseq</SourceDb>
      <SegSetSize>0</SegSetSize>
      <ProjectId>0</ProjectId>
      <Genome>genomic</Genome>

      <SubType>chromosome|map</SubType>
      <SubName>5|5q31-q32</SubName>
      <AssemblyGi>399658</AssemblyGi>
      <AssemblyAcc>D13720.1</AssemblyAcc>
      <Tech/>
      <Completeness/>
      <GeneticCode>1</GeneticCode>

      <Strand/>
      <Organism>Homo sapiens</Organism>
      <Statistics>
        <Stat type="all" count="8"/>
        <Stat type="blob_size" count="16154"/>
        <Stat type="cdregion" count="1"/>
        <Stat type="cdregion" subtype="CDS" count="1"/>
        <Stat type="gene" count="1"/>
        <Stat type="gene" subtype="Gene" count="1"/>
        <Stat type="org" count="1"/>
        <Stat type="prot" count="1"/>
        <Stat type="prot" subtype="Prot" count="1"/>
        <Stat type="pub" count="14"/>
        <Stat type="pub" subtype="PubMed" count="10"/>
        <Stat type="pub" subtype="PubMed/Gene-rif" count="4"/>
        <Stat type="site" count="4"/>
        <Stat type="site" subtype="Site" count="4"/>
        <Stat source="CDD" type="all" count="15"/>
        <Stat source="CDD" type="region" count="6"/>
        <Stat source="CDD" type="region" subtype="Region" count="6"/>
        <Stat source="CDD" type="site" count="9"/>
        <Stat source="CDD" type="site" subtype="Site" count="9"/>
        <Stat source="HPRD" type="all" count="3"/>
        <Stat source="HPRD" type="site" count="3"/>
        <Stat source="HPRD" type="site" subtype="Site" count="3"/>
      </Statistics>
    </DocumentSummary>
  </DocumentSummarySet>
</eSummaryResult>
```

```

    <Stat source="SNP" type="all" count="31"/>
    <Stat source="SNP" type="imp" count="31"/>
    <Stat source="SNP" type="imp" subtype="variation" count="31"/>
    <Stat source="all" type="all" count="57"/>
    <Stat source="all" type="blob_size" count="16154"/>
    <Stat source="all" type="cdregion" count="1"/>
    <Stat source="all" type="gene" count="1"/>
    <Stat source="all" type="imp" count="31"/>
    <Stat source="all" type="org" count="1"/>
    <Stat source="all" type="prot" count="1"/>
    <Stat source="all" type="pub" count="14"/>
    <Stat source="all" type="region" count="6"/>
    <Stat source="all" type="site" count="16"/>
  </Statistics>
  <AccessionVersion>NP_005537.3</AccessionVersion>
  <Properties aa="2">2</Properties>
  <Comment/>
  <OSLT indexed="yes">NP_005537.3</OSLT>
  <IdGiClass mol="3" repr="2" gi_state="10" sat="4" sat_key="58760802"
owner="20"
          sat_name="NCBI" owner_name="NCBI-Genomes" defdiv="GNM" length="620"
extfeatmask="41"
          />
</DocumentSummary>

</DocumentSummarySet>
</eSummaryResult>

```

Downloading Full Records

Basic Downloading

```
efetch.fcgi?db=<database>&id=<uid_list>&rettype=<retrieval_type>
&retmode=<retrieval_mode>
```

Input: List of UIDs (&id); Entrez database (&db); Retrieval type (&rettype); Retrieval mode (&retmode)

Output: Formatted data records as specified

Example: Download nuccore GIs 34577062 and 24475906 in FASTA format

```
https://eutils.ncbi.nlm.nih.gov/entrez/eutils/efetch.fcgi?
db=nuccore&id=34577062,24475906&rettype=fasta&retmode=text
```

Downloading Data From a Previous Search

```
esearch.fcgi?db=<database>&term=<query>&usehistory=y
```

esearch produces WebEnv value (\$web1) and QueryKey value (\$key1)

```
efetch.fcgi?db=<database>&query_key=$key1&WebEnv=$web1&rettype=
<retrieval_type>&retmode=<retrieval_mode>
```

Input: Entrez database (&db); Web environment (&WebEnv) and query key (&query_key) representing a set of Entrez UIDs on the Entrez history server; Retrieval type (&rettype); Retrieval mode (&retmode)

Output: Formatted data records as specified

Downloading a Large Set of Records

Please see [Application 3 in Chapter 3](#)

Input: Entrez database (&db); Web environment (&WebEnv) and query key (&query_key) representing a set of Entrez UIDs on the Entrez history server; Retrieval start (&retstart), the first record of the set to retrieve; Retrieval maximum (&retmax), maximum number of records to retrieve

Output: Formatted data records as specified

For More Information

Please see [EFetch In-Depth](#) for a full description of EFetch.

Finding Related Data Through Entrez Links

Basic Linking

Batch mode – finds only one set of linked UIDs

```
eink.fcgi?dbfrom=<source_db>&db=<destination_db>&id=<uid_list>
```

Input: List of UIDs (&id); Source Entrez database (&dbfrom); Destination Entrez database (&db)

Output: XML containing linked UIDs from source and destination databases

Example: Find one set of Gene IDs linked to nuccore GIs 34577062 and 24475906

<https://eutils.ncbi.nlm.nih.gov/entrez/eutils/eink.fcgi?dbfrom=nuccore&db=gene&id=34577062,24475906>

‘By Id’ mode – finds one set of linked UIDs for each input UID

```
eink.fcgi?dbfrom=<source_db>&db=<destination_db>&id=<uid1>&id=<uid2>&id=<uid3>...
```

Example: Find separate sets of Gene IDs linked to nuccore GIs 34577062 and 24475906

<https://eutils.ncbi.nlm.nih.gov/entrez/eutils/eink.fcgi?dbfrom=nuccore&db=gene&id=34577062&id=24475906>

Note: &db may be a comma-delimited list of databases, so that eink returns multiple sets of linked UIDs in a single call

Finding Links to Data from a Previous Search

```
esearch.fcgi?db=<source_db>&term=<query>&usehistory=y
```

esearch produces WebEnv value (\$web1) and QueryKey value (\$key1)

```
eink.fcgi?dbfrom=<source_db>&db=<destination_db>&query_key=$key1&WebEnv=$web1&cmd=neighbor_history
```

Input: Source Entrez database (&dbfrom); Destination Entrez database (&db); Web environment (&WebEnv) and query key (&query_key) representing the set of source UIDs on the Entrez history server; Command mode (&cmd)

Output: XML containing Web environments and query keys for each set of linked UIDs

Note: To achieve 'By Id' mode, one must send each input UID as a separate &id parameter in the URL. Sending a WebEnv/query_key set always produces Batch mode behavior (one set of linked UIDs).

Finding Computational Neighbors Limited by an Entrez Search

```
eLink.fcgi?dbfrom=<source_db>&db=<source_db>&id=<uid_list>&term=
<query>&cmd=neighbor_history
```

Input: Source Entrez database (&dbfrom); Destination Entrez database (&db); List of UIDs (&id); Entrez query (&term); Command mode (&cmd)

Output: XML containing Web environments and query keys for each set of linked UIDs

Example: Find protein UIDs that are rat Reference Sequences and that are sequence similar to GI 15718680

```
https://eutils.ncbi.nlm.nih.gov/entrez/eutils/eLink.fcgi?
dbfrom=protein&db=protein&id=15718680&term=rat[orgn]
+AND+srcdb+refseq[prop]&cmd=neighbor_history
```

For More Information

Please see [ELink In-Depth](#) for a full description of ELink.

Getting Database Statistics and Search Fields

```
eInfo.fcgi?db=<database>
```

Input: Entrez database (&db)

Output: XML containing database statistics

Note: If no database parameter is supplied, eInfo will return a list of all valid Entrez databases.

Example: Find database statistics for Entrez Protein.

```
https://eutils.ncbi.nlm.nih.gov/entrez/eutils/eInfo.fcgi?db=protein
```

For More Information

Please see [EInfo In-Depth](#) for a full description of EInfo.

Sample EInfo Output

```
<?xml version="1.0"?>
<!DOCTYPE eInfoResult PUBLIC "-//NLM//DTD eInfoResult, 11 May 2002//EN"
"http://www.ncbi.nlm.nih.gov/entrez/query/DTD/eInfo_020511.dtd">
<eInfoResult>
<DbInfo>
<DbName>protein</DbName>
<MenuName>Protein</MenuName>
<Description>Protein sequence record</Description>
<Count>26715092</Count>
<LastUpdate>2009/05/12 04:39</LastUpdate>
<FieldList>
<Field>
<Name>ALL</Name>
<FullName>All Fields</FullName>
<Description>All terms from all searchable fields</Description>
```

```

<TermCount>133639432</TermCount>
<IsDate>N</IsDate>
<IsNumerical>N</IsNumerical>
<SingleToken>N</SingleToken>
<Hierarchy>N</Hierarchy>
<IsHidden>N</IsHidden>
</Field>
...
<Field>
<Name>PORG</Name>
<FullName>Primary Organism</FullName>
<Description>Scientific and common names
of primary organism, and all higher levels of taxonomy</Description>
<TermCount>673555</TermCount>
<IsDate>N</IsDate>
<IsNumerical>N</IsNumerical>
<SingleToken>Y</SingleToken>
<Hierarchy>Y</Hierarchy>
<IsHidden>N</IsHidden>
</Field>
</FieldList>
<LinkList>
<Link>
<Name>protein_biosystems</Name>
<Menu>BioSystem Links</Menu>
<Description>BioSystems</Description>
<DbTo>biosystems</DbTo>
</Link>
...
<Link>
<Name>protein_unigene</Name>
<Menu>UniGene Links</Menu>
<Description>Related UniGene records</Description>
<DbTo>unigene</DbTo>
</Link>
</LinkList>
</DbInfo>
</eInfoResult>

```

Performing a Global Entrez Search

`egquery.fcgi?term=<query>`

Input: Entrez text query (&term)

Output: XML containing the number of hits in each database.

Example: Determine the number of records for mouse in Entrez.

[https://eutils.ncbi.nlm.nih.gov/entrez/eutils/egquery.fcgi?term=mouse\[orgn\]](https://eutils.ncbi.nlm.nih.gov/entrez/eutils/egquery.fcgi?term=mouse[orgn])

For More Information

Please see [EGQuery In-Depth](#) for a full description of EGQuery.

Sample EGQuery Output

```

<?xml version="1.0"?>
<!DOCTYPE Result PUBLIC "-//NLM//DTD eSearchResult, January 2004//EN"

```

```

"https://www.ncbi.nlm.nih.gov/entrez/query/DTD/egquery.dtd">
<!--
    $Id: egquery_template.xml 106311 2007-06-26 14:46:31Z osipov $
-->
<!-- ===== -->
<Result>
  <Term>mouse[orgn]</Term>
  <eGQueryResult>
    <ResultItem>
      <DbName>pubmed</DbName>
      <MenuName>PubMed</MenuName>
      <Count>0</Count>
      <Status>Term or Database is not found</Status>
    </ResultItem>
    <ResultItem>
      <DbName>pmc</DbName>
      <MenuName>PMC</MenuName>
      <Count>3823</Count>
      <Status>Ok</Status>
    </ResultItem>
    ...
    <ResultItem>
      <DbName>nucore</DbName>
      <MenuName>Nucleotide</MenuName>
      <Count>1739903</Count>
      <Status>Ok</Status>
    </ResultItem>
    <ResultItem>
      <DbName>nucgss</DbName>
      <MenuName>GSS</MenuName>
      <Count>2264567</Count>
      <Status>Ok</Status>
    </ResultItem>
    <ResultItem>
      <DbName>nucgst</DbName>
      <MenuName>EST</MenuName>
      <Count>4852140</Count>
      <Status>Ok</Status>
    </ResultItem>
    <ResultItem>
      <DbName>protein</DbName>
      <MenuName>Protein</MenuName>
      <Count>255212</Count>
      <Status>Ok</Status>
    </ResultItem>
    ...
    <ResultItem>
      <DbName>proteinclusters</DbName>
      <MenuName>Protein Clusters</MenuName>
      <Count>13</Count>
      <Status>Ok</Status>
    </ResultItem>
  </eGQueryResult>
</Result>

```

Retrieving Spelling Suggestions

```

espell.fcgi?term=<query>&db=<database>

```

Input: Entrez text query (&term); Entrez database (&db)

Output: XML containing the original query and spelling suggestions.

Example: Find spelling suggestions for the PubMed Central query 'fiberblast cell grwth'.

<https://eutils.ncbi.nlm.nih.gov/entrez/eutils/espell.fcgi?term=fiberblast+cell+grwth&db=pmc>

For More Information

Please see [ESpell In-Depth](#) for a full description of EGQuery.

Sample ESpell Output

```
<?xml version="1.0"?>
<!DOCTYPE eSpellResult PUBLIC "-//NLM//DTD eSpellResult, 23 November
2004//EN" "https://www.ncbi.nlm.nih.gov/entrez/query/DTD/eSpell.dtd">
<eSpellResult>
<Database>pmc</Database>
<Query>fiberblast cell grwth</Query>
<CorrectedQuery>fibroblast cell growth</CorrectedQuery>
<SpelledQuery>
  <Replaced>fibroblast</Replaced>
  <Original> cell </Original>
  <Replaced>growth</Replaced>
</SpelledQuery>
<ERROR/>
</eSpellResult>
```

Demonstration Programs

EBot

EBot is an interactive web tool that first allows users to construct an arbitrary E-utility analysis pipeline and then generates a Perl script to execute the pipeline. The Perl script can be downloaded and executed on any computer with a Perl installation. For more details, see the EBot page linked above.

Sample Perl Scripts

The two sample Perl scripts below demonstrate basic E-utility functions. Both scripts should be copied and saved as plain text files and can be executed on any computer with a Perl installation.

ESearch-EFetch demonstrates basic search and retrieval functions.

```
#!/usr/local/bin/perl -w
# =====
#
#
# PUBLIC DOMAIN NOTICE
# National Center for Biotechnology Information
#
# This software/database is a "United States Government Work" under the
# terms of the United States Copyright Act. It was written as part of
# the author's official duties as a United States Government employee and
# thus cannot be copyrighted. This software/database is freely available
# to the public for use. The National Library of Medicine and the U.S.
# Government have not placed any restriction on its use or reproduction.
#
# Although all reasonable efforts have been taken to ensure the accuracy
```

```

# and reliability of the software and data, the NLM and the U.S.
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#
# =====
#
# Author: Oleg Khovayko
#
# File Description: eSearch/eFetch calling example
#
# -----
# Subroutine to prompt user for variables in the next section

sub ask_user {
    print "$_[0] [$_[1]]: ";
    my $rc = <>;
    chomp $rc;
    if($rc eq "") { $rc = $_[1]; }
    return $rc;
}

# -----
# Define library for the 'get' function used in the next section.
# $utils contains route for the utilities.
# $db, $query, and $report may be supplied by the user when prompted;
# if not answered, default values, will be assigned as shown below.

use LWP::Simple;

my $utils = "https://www.ncbi.nlm.nih.gov/entrez/eutils";

my $db      = ask_user("Database", "Pubmed");
my $query   = ask_user("Query",    "zanzibar");
my $report  = ask_user("Report",   "abstract");

# -----
# $esearch cont?ins the PATH & parameters for the ESearch call
# $esearch_result contains the result of the ESearch call
# the results are displayed and parsed into variables
# $Count, $QueryKey, and $WebEnv for later use and then displayed.

my $esearch = "$utils/esearch.fcgi?" .
    "db=$db&retmax=1&usehistory=y&term=";

my $esearch_result = get($esearch . $query);

print "\nESEARCH RESULT: $esearch_result\n";

$esearch_result =~
    m|<Count>(\d+)</Count>.*<QueryKey>(\d+)</QueryKey>.*<WebEnv>(\S+)</WebEnv>|s;

my $Count      = $1;
my $QueryKey   = $2;
my $WebEnv     = $3;

```

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print "Count = $Count; QueryKey = $QueryKey; WebEnv = $WebEnv\n";

# -----
# this area defines a loop which will display $retmax citation results from
# Efetch each time the the Enter Key is pressed, after a prompt.

my $retstart;
my $retmax=3;

for($retstart = 0; $retstart < $Count; $retstart += $retmax) {
  my $efetch = "$utils/efetch.fcgi?" .
    "rettype=$report&retmode=text&retstart=$retstart&retmax=$retmax&" .
    "db=$db&query_key=$QueryKey&WebEnv=$WebEnv";

  print "\nEF_QUERY=$efetch\n";

  my $efetch_result = get($efetch);

  print "-----\nEFETCH RESULT(" .
    ($retstart + 1) . ".." . ($retstart + $retmax) . "): " .
    "[$efetch_result]\n-----PRESS ENTER!!!-----\n";
  <>;
}

```

EPost-ESummary demonstrates basic uploading and document summary retrieval.

```

#!/usr/local/bin/perl -w
# =====
#
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#
# =====
# Author:  Oleg Khovayko
#
# File Description:  ePost/eSummary calling example
#
# -----
my $utils_root = "https://www.ncbi.nlm.nih.gov/entrez/eutils";

```

```

my $ePost_url      = "$eutils_root/epost.fcgi";
my $eSummary_url  = "$eutils_root/esummary.fcgi";

my $db_name = "PubMed";

# -----
use strict;

use LWP::UserAgent;
use LWP::Simple;
use HTTP::Request;
use HTTP::Headers;
use CGI;

# -----
# Read input file into variable $file
# File name - first argument $ARGV[0]

undef $/; #for load whole file

open IF, $ARGV[0] || die "Can't open for read: $!\n";
my $file = <IF>;
close IF;
print "Loaded file: [$file]\n";

# Prepare file - substitute all separators to comma

$file =~ s/\s+/,/gs;
print "Prepared file: [$file]\n";

#Create CGI param line

my $form_data = "db=$db_name&id=$file";

# -----
# Create HTTP request

my $headers = new HTTP::Headers(
    Accept      => "text/html, text/plain",
    Content_Type => "application/x-www-form-urlencoded"
);

my $request = new HTTP::Request("POST", $ePost_url, $headers );

$request->content($form_data);

# Create the user agent object

my $ua = new LWP::UserAgent;
$ua->agent("ePost/example");

# -----
# send file to ePost by HTTP

my $response = $ua->request($request);

# -----

print "Response status message: [" . $response->message . "]\n";

```

```

print "Response content: [" .          $response->content . "]\n";

# -----
# Parse response->content and extract QueryKey & WebEnv
$response->content =~
  m|<QueryKey>(\d+)</QueryKey>.*<WebEnv>(\S+)</WebEnv>|s;

my $QueryKey = $1;
my $WebEnv   = $2;

print "\nEXTRACTED:\nQueryKey = $QueryKey;\nWebEnv = $WebEnv\n\n";

# -----
# Retrieve DocSum from eSummary by simple::get method and print it
#
print "eSummary result: [" .
  get("$eSummary_url?db=$db_name&query_key=$QueryKey&WebEnv=$WebEnv") .
  "]\n";

```

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Getting Help

Please refer to the [PubMed](#) and [Entrez](#) help documents for more information about search queries, database indexing, field limitations and database content.

Suggestions, comments, and questions specifically relating to the EUtility programs may be sent to entilities@ncbi.nlm.nih.gov.